

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 29, 2002, 20:54:52 ; Search time 1417.73 Seconds
(without alignments)

453.817 Million cell updates/sec

Title: US-09-432-546-15

Sequence: 1 aggaagatgccttggtgccttggaatgcctctatt 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBml:.*
1: gb_ba:.*
2: gb_hlg:.*
3: gb_in:.*
4: gb_om:.*
5: gb_ov:.*
6: gb_pac:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sts:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vl:.*
15: em_ba:.*
16: em_fun:.*
17: em_hum:.*
18: em_in:.*
19: em_om:.*
20: em_or:.*
21: em_ov:.*
22: em_pat:.*
23: em_ph:.*
24: em_pl:.*
25: em_ro:.*
26: em_sts:.*
27: em_sy:.*
28: em_un:.*
29: em_vl:.*
30: em_hlg_hum:.*
31: em_hlg_in:.*
32: em_hlg_rod:.*
33: em_hlg_hum:.*
34: em_hlg_in:.*
35: em_hlg_rod:.*
36: em_hlg_other:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24.6	63.1	178904	2	AL354989 Homo sapi
C 2	24.6	63.1	184748	2	AL160051 Homo sapi
C 3	24.2	62.1	67982	2	AC068869 Homo sapi
C 4	24.2	62.1	107839	2	AP000574 Homo sapi
C 5	24.2	62.1	114478	2	AP000489 Homo sapi
C 6	24.2	62.1	123500	2	AP000406 Homo sapi
C 7	24.2	62.1	128206	2	AP001258 Homo sapi
C 8	24.2	62.1	1225142	2	AP002358 Homo sapi
C 9	24.2	61.1	226020	2	AC087689 Homo sapi
C 10	24	61.5	195496	2	AL360214 Homo sapi
C 11	24	61.5	203257	9	AC013737 Homo sapi
C 12	23.8	61.0	1752	10	AF244362 Mus muscu
C 13	23.2	59.5	49743	2	AC017211 Drosophi
C 14	23.2	59.5	198721	2	AC010060 Drosophi
C 15	23.2	59.5	274585	3	AE003533 Drosophi
C 16	23	59.0	5767	10	DB3002 Mouse mR
C 17	23	59.0	12485	1	AE004962 Pseudom
C 18	23	59.0	68790	2	HSJ287H17 Human
C 19	23	59.0	136117	2	AC008700 Homo sapi
C 20	23	59.0	182127	2	AP001842 Homo sapi
C 21	23	59.0	184284	2	AC025582 Mus muscu
C 22	23	59.0	192110	2	AP004070 Oryza sat
C 23	23	59.0	226899	2	AL596188 Homo sapi
C 24	22.8	58.5	130192	9	AL157832 Human
C 25	22.8	58.5	157058	2	AL353725 Homo sapi
C 26	22.8	58.5	187344	2	AL354873 Human
C 27	22.6	57.9	174253	9	AC068590 Homo sapi
C 28	22.4	57.4	1148	9	MFNADIDGS X74124 M. fascicula
C 29	22.4	57.4	1285	9	HSJ69268 Human
C 30	22.4	57.4	1343	9	BC001902 Homo sapi
C 31	22.4	57.4	1362	9	BC000933 Homo sapi
C 32	22.4	57.4	1370	9	HSRMAIDH BC000933 Homo sapi
C 33	22.4	57.4	1506	9	HSU40272 Human
C 34	22.4	57.4	18234	9	HSIDHTRAP Z68129 H. sapiens
C 35	22.4	57.4	191923	9	AC087886 Homo sapi
C 36	22.4	57.4	230516	9	HSU52111 H. sapien
C 37	22.2	56.9	131600	2	AC019859 Drosophi
C 38	22.2	56.9	151162	9	AC009364 Human
C 39	22.2	56.9	156508	3	AC007581 Drosophi
C 40	22.2	56.9	158648	2	AC021853 Homo sapi
C 41	22.2	56.9	170089	3	AC007925 Drosophi
C 42	22.2	56.9	188090	9	AC011625 Homo sapi
C 43	22.2	56.9	306848	3	AE003464 Drosophi
C 44	22	56.4	123386	8	FI2F1 Arabidops
C 45	22	56.4	134331	2	AL603727 Rattus no

ALIGNMENTS

RESULT 1
AL354989/c
LOCUS
DEFINITION Homo sapiens chromosome 9 clone RP11-537H15, *** SEQUENCING IN
PROGRESS ***; 2 unordered pieces.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AL354989 178904 bp DNA HTG 02-AUG-2001
AL354989.8 GI:15131225
HTG; HTGS_PHAESA; HTGS_ACTIVERIN; HTGS_DRAFT; HTGS_FULLTOP.
human.
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 178904)

REFERENCE
AUTHORS
TITLE
JOURNAL
Chapman, J.
Direct Submission
Submitted (01-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk

REQUESTS: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:14715324.
----- Genome Center

COMMENT


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misc_feature /note="assembly_fragment:04097  
fragment_chain:1"  
13182..16296  
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166668..173995  
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/note="assembly_fragment:03195"  
181511..184748  
/note="assembly_fragment:03517"
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[illegible]

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

1 (bases 1 to 67982)
Birtten, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-753E17
Unpublished
2 (bases 1 to 67982)
Birtten, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,
Campiano, A., Castle, A., Choerel, Y., Colangelo, M., Collins, S.,
Collumore, A., Cooke, P., Dakrellano, K., Dewar, K., Diaz, J. S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galaan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heiford, A., Horton, L.,
Howard, J. C., Iliev, I., Johnson, R., Jones, C., Kam, L., Kartas, A.,
Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lebochzy, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N.,
McCarthy, M., McKean, P., McGuirk, A., McKernan, C., McPheters, R.,
Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mlenka, V., Morrow,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Ollivar, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schaner, S., Severy, P., Spencer, B.,
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testaye, S., Theodore, J., Tifrel, A., Travers, M., Trifillo, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (10-MAY-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
Genome Center

Center Whitehead Institute/ MIT Center for Genome Research
Center code: WIMR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L9390
Center clone name: 753_E_17

* NOTE: this record contains 93 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

*	1	646:	contlg of 646 bp	in length
*	647	746:	gap of 100 bp	
*	747:	1363:	contlg of 617 bp	in length
*	1364	1463:	gap of 100 bp	
*	1464	2072:	contlg of 609 bp	in length
*	2073	2172:	gap of 100 bp	
*	2173	2806:	contlg of 634 bp	in length
*	2807	2806:	gap of 100 bp	
*	2907	3536:	contlg of 630 bp	in length
*	3537	3636:	gap of 100 bp	
*	3637	4233:	contlg of 357 bp	in length
*	4234	4333:	gap of 100 bp	
*	4334	4970:	contlg of 637 bp	in length
*	4971	5070:	gap of 100 bp	
*	5071	5668:	contlg of 598 bp	in length
*	5669	5768:	gap of 100 bp	
*	5769	6382:	contlg of 614 bp	in length
*	6383	6482:	gap of 100 bp	
*	6483	7124:	contlg of 642 bp	in length
*	7125	7224:	gap of 100 bp	
*	7225	7858:	contlg of 634 bp	in length

```

* 7859 7958: gap of 100 bp
* 7959 8603: contig of 645 bp in length
* 8604 8703: gap of 100 bp
* 9351 9450: contig of 647 bp in length
* 9451 10065: contig of 100 bp
* 10066 10165: gap of 100 bp
* 10166 10797: contig of 632 bp in length
* 10798 10897: gap of 100 bp
* 10898 11522: contig of 625 bp in length
* 11523 11622: gap of 100 bp
* 11623 12251: contig of 629 bp in length
* 12252 12351: gap of 100 bp
* 12352 12988: contig of 637 bp in length
* 12989 13088: gap of 100 bp
* 13089 13708: contig of 620 bp in length
* 13709 13808: gap of 100 bp
* 13809 14453: contig of 645 bp in length
* 14454 14553: gap of 100 bp
* 14554 15193: contig of 640 bp in length
* 15194 15293: gap of 100 bp
* 15294 15925: contig of 632 bp in length
* 15926 16025: gap of 100 bp
* 16026 16640: contig of 615 bp in length
* 16641 16740: gap of 100 bp
* 16741 17378: contig of 638 bp in length
* 17379 17478: gap of 100 bp
* 17479 18084: contig of 606 bp in length
* 18085 18184: gap of 100 bp
* 18185 18825: contig of 641 bp in length
* 18826 18925: gap of 100 bp
* 18926 19545: contig of 620 bp in length
* 19546 19645: gap of 100 bp
* 20304 20403: contig of 658 bp in length
* 20404 21035: gap of 100 bp
* 21036 21135: contig of 632 bp in length
* 21136 21796: contig of 661 bp in length
* 21797 21896: gap of 100 bp
* 21897 22533: contig of 637 bp in length
* 22534 22633: gap of 100 bp
* 22634 23256: contig of 623 bp in length
* 23257 23356: gap of 100 bp
* 23357 24007: contig of 651 bp in length
* 24008 24107: gap of 100 bp
* 24108 24751: contig of 644 bp in length
* 24752 24851: gap of 100 bp
* 24852 25480: contig of 629 bp in length
* 25481 25580: gap of 100 bp
* 25581 26192: contig of 612 bp in length
* 26193 26292: gap of 100 bp
* 26293 26899: contig of 607 bp in length
* 26900 26999: gap of 100 bp
* 27000 27609: contig of 610 bp in length
* 27610 27709: gap of 100 bp
* 27710 28333: contig of 624 bp in length
* 28334 28433: gap of 100 bp
* 28434 29067: contig of 634 bp in length
* 29068 29167: gap of 100 bp
* 29168 29822: contig of 655 bp in length
* 29823 29922: gap of 100 bp
* 29923 30589: contig of 667 bp in length
* 30590 30689: gap of 100 bp
* 30690 31333: contig of 644 bp in length
* 31334 31433: gap of 100 bp
* 31434 32076: contig of 643 bp in length
* 32077 32176: gap of 100 bp
* 32177 32817: contig of 641 bp in length
* 32818 32917: gap of 100 bp
* 32918 33544: contig of 627 bp in length
* 33545 33644: gap of 100 bp
* 33645 34293: contig of 649 bp in length
* 34294 34393: gap of 100 bp

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* 34394 35026: contig of 633 bp in length
* 35027 35126: gap of 100 bp
* 35127 35768: contig of 642 bp in length
* 35769 35868: gap of 100 bp
* 35869 36482: contig of 614 bp in length
* 36483 36582: gap of 100 bp
* 36583 37227: contig of 645 bp in length
* 37228 37327: gap of 100 bp
* 37328 37950: contig of 623 bp in length
* 37951 38050: gap of 100 bp
* 38051 38667: contig of 617 bp in length
* 38668 38767: gap of 100 bp
* 38768 39395: contig of 628 bp in length
* 39396 39495: gap of 100 bp
* 39496 40140: contig of 645 bp in length
* 40141 40240: gap of 100 bp
* 40241 40881: contig of 641 bp in length
* 40882 40981: gap of 100 bp
* 40982 41626: contig of 645 bp in length
* 41627 41726: gap of 100 bp
* 41727 42373: contig of 647 bp in length
* 42374 42473: gap of 100 bp
* 42474 43094: contig of 621 bp in length
* 43095 43194: gap of 100 bp
* 43195 43805: contig of 611 bp in length
* 43806 43905: gap of 100 bp
* 43906 44535: contig of 630 bp in length
* 44536 44635: gap of 100 bp
* 44636 45279: contig of 644 bp in length
* 45280 45379: gap of 100 bp
* 45380 46013: contig of 634 bp in length
* 46014 46113: gap of 100 bp
* 46114 46716: contig of 603 bp in length
* 46717 46816: gap of 100 bp
* 46817 47451: contig of 635 bp in length
* 47452 47551: gap of 100 bp
* 47552 48197: contig of 646 bp in length
* 48198 48297: gap of 100 bp
* 48298 48927: contig of 630 bp in length
* 48928 49027: gap of 100 bp
* 49028 49660: contig of 633 bp in length
* 49661 49760: gap of 100 bp
* 49761 50383: contig of 623 bp in length
* 50384 50483: gap of 100 bp

Query Match      62.1%; Score 24.2; DB 2; Length 67982;
Best Local Similarity 78.4%; Pred. No. 37;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 1 agagatgcctgtgtgcttgaatgccttc 37
Db 63244 AGTAGTGCGCAATGTCTCTAGGAATGCGCTCTGA 63208

RESULT 4
AP000574/c
LOCUS
DEFINITION
Homo sapiens chromosome 11 clone CMB9-49B9 map 11q12, WORKING DRAFT
SEQUENCE 9 unordered pieces.
ACCESSION
AP000574
VERSION
AP000574.2 GI:8118782
KEYWORDS
HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens DNA, clone: CMB9-49B9.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 107839)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 107,839 genomic DNA of 11q12
Published Only in Database (1999) In press
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 107839)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

```

Chemistry: Dye-terminator ET-amersham sequencing vector; PCR products; 100%

1. *What is the purpose of this study?*

Assembly program: Phrap; version 0.990329
 Consensus quality: 109628 bases at least Q40
 Consensus quality: 112052 bases at least Q30
 Consensus quality: 113108 bases at least Q20
 Insert size: 113678; sum-of-ctrls
 Quality coverage: 6.65x in Q20 bases; sum-of-ctrls

NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 58724 contig of 58724 bp in length
 58825 83984 contig of 25160 bp in length
 84085 95379 contig of 11295 bp in length
 95480 105075 contig of 9596 bp in length
 105176 111400 contig of 6325 bp in length
 111501 113358 contig of 1838 bp in length
 113439 114478 contig of 1040 bp in length

Sequence updated (04-Nov-1999)
 Sequence updated (26-May-2000):

* NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 58724: contig of 58724 bp in length
 58725 58824: gap of 100 bp
 58825 83984: contig of 25160 bp in length
 83985 84084: gap of 100 bp
 84085 95379: contig of 11295 bp in length
 95380 95479: gap of 100 bp
 95480 105075: contig of 9596 bp in length
 105076 105175: gap of 100 bp
 105176 111400: contig of 6225 bp in length
 111401 111500: gap of 100 bp
 111501 113358: contig of 1838 bp in length
 113359 113438: gap of 100 bp
 113439 114478: contig of 1040 bp in length.

FEATURES

source

1. 114478
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 /db_xref="taxon:9606"
 /chromosome="11"
 /map="11q13"
 /clone="CMB9-7F5"
 1. 58724
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 58825. 83984
 /note="assembly-fragment clone_end:17 vector_side:left"
 84085. 95379
 /note="assembly-fragment"
 95480. 105075
 /note="assembly-fragment"
 105176. 111400
 /note="assembly-fragment clone_end:SP6 vector_side:right"
 111501. 113358
 /note="assembly-fragment"
 113439. 114478
 /note="assembly-fragment"
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 BASE COUNT
 ORIGIN

Query Match 62.1%; Score 24.2; DB 2; Length 114478;
 Best Local Similarity 78.4%; Pred. No. 37;
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 agagatggccttggtgagccttggaatgacctcta 37
 ||||| ||||| ||||| ||||| ||||| |||||
 Db 54667 AATGATGGCAATGTTCTTCTAGGAATGGCTCTGGA 54631

RESULT 6
 AP000406/c
 LOCUS
 DEFINITION
 Homo sapiens chromosome 11 clone CMB9-21D9 map 11q12, WORKING DRAFT SEQUENCE, 4 unordered pieces.
 AP000406
 ACCESSION
 AP000406.4 GI:9927270
 VERSION
 HTG; HTGS; PHASE1; HTGS; DRAFT.
 KEYWORDS
 Homo sapiens DNA, clone:CMB9-21D9.
 SOURCE
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 123300)
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 Homo sapiens 123,300 genomic DNA of 11q12
 Published Only in Database (1999) In press
 2 (bases 1 to 123300)
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 Direct Submission
 Submitted (27-AUG-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-15-1 Kitarato, Sagamihara, Kanagawa 228-8555, Japan
 (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
 On Aug 26, 2000 this sequence version replaced gi:8118745.

COMMENT

Center: RIKEN Genomic Sciences Center (GSC)

Center code: RIKEN

Web site: http://hgp.gsc.riken.go.jp/

Contact: hattori@gsc.riken.go.jp

Project Information

Center project name: HumDrafit1

Center clone name: CMB9-21D9

Summary Statistics

Sequencing vector: PCR products; 100% of reads

Chemistry: Dye-terminator ET-amersham; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 121846 bases at least Q40

Consensus quality: 122507 bases at least Q30

Consensus quality: 122832 bases at least Q20

Insert size: 123000; sum-of-ctrls

Quality coverage: 13.07x in Q20 bases; sum-of-ctrls

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 61533 contig of 61533 bp in length
 61634 106881 contig of 45248 bp in length
 106982 119565 contig of 12584 bp in length
 119666 123300 contig of 3635 bp in length.

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 61533: contig of 61533 bp in length
 61634 61633: gap of 100 bp
 61634 106881: contig of 45248 bp in length
 106882 106981: gap of 100 bp

```

FEATURES
  * 106982 119565: contig of 12584 bp in length
  * 119566 119665: gap of 100 bp
  * 119666 123300: contig of 3635 bp in length.
    Location/Qualifiers
      1. 123300
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         /db_xref="taxon:9606"
         /chromosome="11"
         /map="11q12"
         /clone="CMB9-21D9"
      misc_feature
        1. 61533
           /note="assembly-fragment"
      misc_feature
        61634..106881
           /note="assembly-fragment"
      misc_feature
        106982..119565
           /note="assembly-fragment clone_end:SP6 vector_side:right"
      misc_feature
        119666..123300
           /note="assembly-fragment clone_end:T7 vector_side:right"
BASE COUNT  36534 a 25670 c 26307 g 34489 t 300 others
ORIGIN
Query Match      62.1%; Score 24.2; DB 2; Length 123300;
Best Local Similarity 78.4%; Pred. No. 37;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 aggaatgacctgtgcttggaatgacctctta 37
    ||||| ||||| ||||| ||||| ||||| |||||
Db 48009 AGTAGGTGCAGATGTCTCTAGGAATGCGCTCTGA 47973

RESULT 7
AP001258/c 128206 bp DNA HTG 07-OCT-2000
LOCUS Homo sapiens chromosome 11 clone CMB9-103D1 map 11q12, WORKING
DEFINITION DRAFT SEQUENCE, 4 unordered pieces.
ACCESSION AP001258 GI:10716815
VERSION HTG: HTGS_PHASE1; HTGS-DRAFT.
KEYWORDS Homo sapiens DNA, clone:CMB9-103D1.
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 128206)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 128,206 genomic DNA of 11q12
TITLE Published Only in Database (2000) In press
JOURNAL 2 (bases 1 to 128206)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (23-FEB-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-42-778-9923, Fax:81-42-778-9924)
On Oct 7, 2000 this sequence version replaced gi:8117651.
COMMENT
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraft11
Center clone name: CMB9-103D1
----- Summary Statistics
Sequencing vector: PCR products: 100% of reads
Chemistry: Dye-terminator ET-amersham: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 126341 bases at least Q40
Consensus quality: 127174 bases at least Q30
Consensus quality: 127641 bases at least Q20

```

```

Insert size: 127906; sum-of-contigs
Quality coverage: 9.70x in Q20 bases; sum-of-contigs
-----
NOTE: This is a 'working draft' sequence. It currently consists of
4 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved.
1 89511 contig of 89511 bp in length
89612 107913 contig of 18302 bp in length
108014 119129 contig of 11116 bp in length
119230 128206 contig of 8977 bp in length.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 89511: contig of 89511 bp in length
* 89512 89611: gap of 100 bp
* 89612 107913: contig of 18302 bp in length
* 107914 108013: gap of 100 bp
* 108014 119129: contig of 11116 bp in length
* 119130 119229: gap of 100 bp
* 119230 128206: contig of 8977 bp in length.
FEATURES
  Location/Qualifiers
    1. 128206
       /organism="Homo sapiens"
       /db_xref="taxon:9606"
       /chromosome="11"
       /map="11q12"
       /clone="CMB9-103D1"
    misc_feature
      1..89511
         /note="assembly-fragment clone_end:T7 vector_side:left"
    misc_feature
      89612..107913
         /note="assembly-fragment"
    misc_feature
      108014..119129
         /note="assembly-fragment clone_end:SP6 vector_side:left"
    misc_feature
      119230..128206
         /note="assembly-fragment"
BASE COUNT  37466 a 26270 c 26422 g 37748 t 300 others
ORIGIN
Query Match      62.1%; Score 24.2; DB 2; Length 128206;
Best Local Similarity 78.4%; Pred. No. 37;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 aggaatgacctgtgcttggaatgacctctta 37
    ||||| ||||| ||||| ||||| ||||| |||||
Db 94422 AGTAGGTGCAGATGTCTCTAGGAATGCGCTCTGA 94386

RESULT 8
AP002358 225142 bp DNA HTG 13-JAN-2001
LOCUS Homo sapiens chromosome 11 clone RP11-1036E20 map 11q, WORKING
DEFINITION DRAFT SEQUENCE, 13 unordered pieces.
ACCESSION AP002358 GI:12225034
VERSION HTG: HTGS_PHASE1; HTGS-DRAFT.
KEYWORDS Homo sapiens DNA, clone:RP11-1036E20.
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 225142)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 225,142 genomic DNA of 11q

```

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Published Only in Database (2000) In press
2 (bases 1 to 225142)

Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@gscc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
On Jan 13, 2001 this sequence version replaced g1:8131622.

COMMENT

Genome Center

Center: RIKEN Genomic Sciences Center (GSC)

Center code: RIKEN

Web site: http://hgp.gsc.riken.go.jp/

Contact: hattori@gscc.riken.go.jp

Project Information

Center project name: HumDraTcl1

Center clone name: RP11-1036E20

Summary Statistics

Sequencing vector: PCR products; 100% of reads

Chemistry: Dye-terminator EM-amersham; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 219245 bases at least Q40

Consensus quality: 222418 bases at least Q30

Insert size: 223942; sum-of-contigs

Quality coverage: 8.03x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
13 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved

1 55748 contig of 55748 bp in length
55849 81106 contig of 25258 bp in length
105144 129107 contig of 23837 bp in length
129208 149114 contig of 23964 bp in length
149215 165167 contig of 19907 bp in length
165167 182204 contig of 16302 bp in length
182204 192999 contig of 16588 bp in length
192999 203328 contig of 10695 bp in length
203328 208865 contig of 10229 bp in length
208865 216574 contig of 5437 bp in length
216574 222800 contig of 7609 bp in length
222800 225142 contig of 6126 bp in length
225142 22901 contig of 2242 bp in length.

NOTE: This is a 'working draft' sequence. It currently
consists of 13 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 55748: contig of 55748 bp in length
55749 55848: gap of 100 bp
55849 81106: contig of 25258 bp in length
81107 81206: gap of 100 bp
81207 105043: contig of 23837 bp in length
105044 105143: gap of 100 bp
105144 129107: contig of 23964 bp in length
129108 129207: gap of 100 bp
129208 149114: contig of 19907 bp in length
149115 149214: gap of 100 bp
149215 165166: contig of 16302 bp in length
165167 165167: gap of 100 bp
165167 182204: contig of 16588 bp in length
182205 182304: gap of 100 bp
182305 192999: contig of 10695 bp in length
193000 193099: gap of 100 bp

FEATURES

source

* 193100 203328: contig of 10229 bp in length
* 203329 203428: gap of 100 bp
* 203429 208865: contig of 5437 bp in length
* 208866 208965: gap of 100 bp
* 208966 216574: contig of 7609 bp in length
* 216575 216674: gap of 100 bp
* 216675 222800: contig of 6126 bp in length
* 222801 222900: gap of 100 bp
* 222901 225142: contig of 2242 bp in length.

Location/Qualifiers

1. 225142

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="11"

/map="11g"

/clone="RP11-1036E20"

1. 55748

/note="assembly-fragment clone_end:SP6 vector_side:right"

55849..81106

/note="assembly-fragment"

81207..105043

/note="assembly-fragment"

105144..129107

/note="assembly-fragment"

129208..149114

/note="assembly-fragment"

149215..165166

/note="assembly-fragment"

165167..182204

/note="assembly-fragment"

182305..192999

/note="assembly-fragment"

193100..203328

/note="assembly-fragment"

203429..208865

/note="assembly-fragment"

208966..216574

/note="assembly-fragment clone_end:T7 vector_side:left"

216675..222800

/note="assembly-fragment"

222901..225142

/note="assembly-fragment"

22901..46820 c 47221 g 66847 t 1200 others

BASE COUNT 63054 a 46820 c 47221 g 66847 t 1200 others

ORIGIN

Query Match 62.1%; Score 24.2; DB 2; Length 225142;

Best Local Similarity 78.4%; Pred. No. 37;

Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 agagatggcctgtgtgcttgaatgctctta 37

Db 188212 AGTAGTGCGCATGTGTCTAGGAATGCTCTGA 188248

RESULT 9

AC087689 226020 bp DNA HTG 27-MAY-2001

LOCUS Homo sapiens chromosome 11 clone RP11-1036E20 map 11, WORKING DRAFT

DEFINITION AC087689 9 unordered pieces.

ACCESSION AC087689 3 GI:14210561

VERSION HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 226020)

Bioren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 11, clone RP11-1036E20

Unpublished

JOURNAL 2 (bases 1 to 226020)

Bioren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Grinde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karates, A., Laroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., MacDonald, P., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J., Meneus, E., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Plunkhang, P., Pierre, N., Pollard, V., Raymond, C., Retta, R., Ribbeck, M., Riley, R., Rise, C., Rogov, P., Roman, P., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Sudramanian, A., Talamas, J., Testaye, S., Theodore, J., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zahoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (15-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 27, 2001 this sequence version replaced gi:13123260.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L12345
Center clone name: 1036_E_20

Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 221473 bases at least Q40
Consensus quality: 222976 bases at least Q30
Consensus quality: 223564 bases at least Q20
Insert size: 224000; agarose-fp
Insert size: 225220; sum-of-coverage
Quality coverage: 8.7 in Q20 bases; agarose-fp
Quality coverage: 8.7 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 2472: contig of 2472 bp in length
2473 2572: gap of 100 bp
2573 3289: contig of 717 bp in length
3290 3389: gap of 100 bp
3390 4086: contig of 697 bp in length
4087 4186: gap of 100 bp
4187 5709: contig of 1523 bp in length
5710 5809: gap of 100 bp
5810 17972: contig of 12163 bp in length
17973 18072: gap of 100 bp
18073 45215: contig of 27143 bp in length
45216 45315: gap of 100 bp
45316 92283: contig of 46968 bp in length
92284 92383: gap of 100 bp
92384 156424: contig of 64041 bp in length
156425 156524: gap of 100 bp
156525 226020: contig of 69496 bp in length.
Location/Qualifiers

source 1..226020
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-1036E20"
/clone_lib="RPC1-11 Human Male BAC"
1..2472
/note="assembly-fragment
clone_end:SP6
vector_side:left"
misc_feature 2573..3289
/note="assembly-fragment"
3390..4086
/note="assembly-fragment"
4187..5709
/note="assembly-fragment"
5810..17972
/note="assembly-fragment"
18073..45215
/note="assembly-fragment"
45316..92283
/note="assembly-fragment"
92384..156424
/note="assembly-fragment"
156525..226020
/note="assembly-fragment
clone_end:T7
vector_side:right"
BASE COUNT 66670 a 47794 c 46268 g 64486 t 802 others
ORIGIN

Query Match 62.1%; Score 24.2; DB 2; Length 226020;
Best Local Similarity 78.4%; Pred. No. 37;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY 1 aggagatgccttgctgcttgaatgctctta 37
Db 215819 AGTAGTGCGCATGTGTCTTAGGAATGCGCTCTGA 215855

RESULT 10
AL360214/c DNA HTG 04-AUG-2001
LOCUS
DEFINITION Homo sapiens chromosome 10 clone RP11-533N1, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
ACCESSION AL360214
VERSION AL360214.18 GI:15131258
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVIFIERIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 195496)
REFERENCE
AUTHORS Chapman, J.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
REQUESTS: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:15028671.
COMMENT
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: ba533N7
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: Plasmid; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 194004 bases at least Q40

Consensus quality: 194462 bases at least Q30
 Consensus quality: 194743 bases at least Q20
 Insert size: 195396; sum-of-contigs
 Insert size: 179111; 5.5% error; agarose-fp
 Quality coverage: 7.28x in Q20 bases; sum-of-contigs quality
 coverage: 8.01x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved

* 1 103853: contig of 103853 bp in length
 * 103854 103953: gap of 100 bp
 * 103954 195496: contig of 91543 bp in length.
 Location/Qualifiers

FEATURES
 source
 1. 195496

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="10"

misc_feature
 1. 103853
 /clone.lib="RPC1-11.2"

/note="assembly_fragment:03932
 fragment_chain:1"

misc_feature
 103954..195496
 /note="assembly_fragment:03176
 fragment_chain:1"

BASE COUNT 66183 a 33423 c 33235 g 62555 t 100 others
 ORIGIN

Query Match 61.5%; Score 24; DB 2; Length 195496;
 Best Local Similarity 84.4%; Pred. No. 45;
 Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 atggccttggtgcttggaatgacctcta 37
 || ||||| ||||| ||||| ||||| |||||
 DB 676 ATTCCCTTGCTGCGCTTGATTTGGCTCTTA 645

RESULT 11
 AC013737/c 203257 bp DNA PRI 18-JAN-2001
 LOCUS AC013737 Homo sapiens chromosome 10 clone RP11-313B15, complete sequence.
 DEFINITION AC013737
 AC013737.4 GI:7715619
 HTG.
 KEYWORDS human.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 203257)
 Smith, D.R.
 TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
 Sequence Data
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 203257)
 Smith, D.R.
 TITLE Direct Submission
 JOURNAL Submitted (15-NOV-1999) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 REFERENCE 3 (bases 1 to 203257)
 Smith, D.R.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAY-2000) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 REFERENCE 4 (bases 1 to 203257)
 Smith, D.R.
 TITLE Direct Submission

JOURNAL Submitted (15-JUN-2000) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA
 REFERENCE 5 (bases 1 to 203257)
 Smith, D.R.
 TITLE Direct Submission
 JOURNAL Submitted (18-JAN-2001) Genome Therapeutics Corporation, 100 Beaver
 Street, Waltham, MA 02453, USA

COMMENT On May 7, 2000 this sequence version replaced gi:6539205.
 FEATURES
 source
 1. 203257
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="10"

/clone.lib="RPC1-11"
 /clone.lib="RPC1-11"

BASE COUNT 68225 a 36293 c 35286 g 63453 t
 ORIGIN

Query Match 61.5%; Score 24; DB 9; Length 203257;
 Best Local Similarity 84.4%; Pred. No. 45;
 Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 atggccttggtgcttggaatgacctcta 37
 || ||||| ||||| ||||| ||||| |||||
 DB 144662 ATTCCCTTGCTGCGCTTGATTTGGCTCTTA 144631

RESULT 12
 AF244362 1752 bp mRNA ROD 30-SEP-2000
 LOCUS AF244362 Mus musculus ubiquitin-protein ligase UBE3B (ube3b) mRNA, partial
 cds.
 DEFINITION AF244362
 AF244362.1 GI:10436098
 VERSION
 KEYWORDS house mouse.
 SOURCE
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1752)
 Lomax, M.I., Huang, L., Choab, Y., Gonga, T.L. and Altschuler, R.A.
 TITLE Differential display and gene arrays to examine auditory plasticity
 JOURNAL Hear. Res. 147 (1-2), 293-302 (2000)
 MEDLINE 20420030
 REFERENCE 2 (bases 1 to 1752)
 Lomax, M.I. and Huang, L.
 AUTHORS Direct Submission
 TITLE Submitted (10-MAR-2000) Dept. of Otolaryngology, Kresge Hearing
 Research Institute, 1150 W. Med. Ctr. Dr., Ann Arbor, MI 48109, USA
 JOURNAL Location/Qualifiers

FEATURES
 source
 1. 1752
 /organism="Mus musculus"
 /strain="C57BL/6/J"
 /db_xref="taxon:10090"
 /clone.lib="IMAGE:352315"
 /dev_stage="embryo"
 <1. 1752
 /gene="ube3b"
 <1. 583
 /gene="ube3b"
 /codon_start=2
 /product="ubiquitin-protein ligase UBE3B"
 /protein_id="AA016783.1"
 /db_xref="GI:10436098"
 /translation="KISYIHLMHFRNHTQIKQNTALISGRSITKPKWIKFSTPE
 LQRTISDNAMEIDLEDLKRHYVGGFGHSHRVILWMDILASDFPERRAFNLKFT
 SCGRPLIGFAVILKPPSIRCVESDODGTGLVGLGFTIRRRBGRPLPTST
 CFNLKLPNSKSVLRERKRVASIMNTGELS"

BASE COUNT 412 a 469 c 454 g 417 t
 ORIGIN


```

* 92681 92780: gap of unknown length
* 92781 98832: contig of 6052 bp in length
* 98833 98832: gap of unknown length
* 98833 103033: contig of 4101 bp in length
* 103033 103133: gap of unknown length
* 103133 105829: contig of 2696 bp in length
* 105829 105830: gap of unknown length
* 105830 109921: contig of 3992 bp in length
* 109921 110022: gap of unknown length
* 110022 113287: contig of 3266 bp in length
* 113287 113387: gap of unknown length
* 113387 117302: contig of 3915 bp in length
* 117302 117402: gap of unknown length
* 117402 120658: contig of 3256 bp in length
* 120658 120759: gap of unknown length
* 120759 123618: contig of 2859 bp in length
* 123618 123717: gap of unknown length
* 123717 126754: contig of 3037 bp in length
* 126754 126854: gap of unknown length
* 126854 129310: contig of 2456 bp in length
* 129310 129411: gap of unknown length
* 129411 132040: contig of 2630 bp in length
* 132040 132140: gap of unknown length
* 132140 134668: contig of 2528 bp in length
* 134668 134768: gap of unknown length
* 134768 137836: contig of 3068 bp in length
* 137836 137936: gap of unknown length
* 137936 139970: contig of 2034 bp in length
* 139970 140070: gap of unknown length
* 140070 141985: contig of 1915 bp in length
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Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O.,
Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
Science 287 (5461), 2185-2195 (2000)
20196006
TITLE
JOURNAL
MEDLINE
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AUTHORS
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TITLE
- COMMENT
FEATURES
SOURCE
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Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
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Rockville, MD, USA
On Oct 9, 2000 this sequence version replaced gi:7294349.
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